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JUL 29 2003

TECH CENTER I509482C



1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/509,482C

DATE: 07/24/2003

TIME: 08:06:52

Input Set : E:\SEQLIST.txt

Output Set: N:\CRF4\07242003\I509482C.raw

4 <110> APPLICANT: Crofts, Linda Anne
 5 Hancock, Manuela S.
 6 Morrison, Nigel A.
 7 Eisman, John A.
 9 <120> TITLE OF INVENTION: Isoforms of the Human Vitamin D Receptor
 12 <130> FILE REFERENCE: RICE-014
 14 <140> CURRENT APPLICATION NUMBER: 09/509,482C
 15 <141> CURRENT FILING DATE: 2000-09-15
 17 <150> PRIOR APPLICATION NUMBER: PCT/AU98/00817
 18 <151> PRIOR FILING DATE: 1998-09-29
 20 <150> PRIOR APPLICATION NUMBER: P09500
 21 <151> PRIOR FILING DATE: 1997-09-29
 23 <160> NUMBER OF SEQ ID NOS: 21
 25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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 29 <212> TYPE: DNA
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 38 <212> TYPE: DNA
 39 <213> ORGANISM: Homo sapiens
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 44 tgagacctca cagaagagca cccctgggct ccacttacct gccccctgct ccttcaggga 180
 45 tggaggcaat ggcgccagc acttccctgc ctgaccctgg agactttgac cggaacgtgc 240
 46 cccgatctg tggggtgtgt ggagaccgag ccactggctt tcaacttcaat gctatgacct 300
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 48 ccttcaacgg ggactgccgc atcaccaagg acaaccgacg ccactgccag gcctgccggc 420
 49 tcaaagctg tgtggacatc ggcgatgatga aggagtcat tctgacagat gaggaagtgc 480
 50 agaggaagcg ggagatgatc ctgaagcgga aggaggagga ggccttgaag gacagtctgc 540
 51 ggcccaagct gtctgaggag cagcagcgca tcattgccat actgctggac gccaccata 600
 52 agacctacga cccacctac tccgacttct gccagttccg gcctccagtt cgtgtgaatg 660
 53 atggtggagg gagccatcct tccaggccca actccagaca cactccagc ttctctgggg 720
 54 actcctctc ctctgtctca gatcactgta tcacctcttc agacatgatg gactcgtcca 780
 55 gcttctccaa tctggatctg agtgaagaag attcagatga cccttctgtg accctagagc 840
 56 tgtcccagct ctccatgctg cccacctgg ctgacctggt cagttacagc atccaaaagg 900
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59 tggacgacat gtcctggacc tgtggcaacc aagactacaa gtaccgcgctc agtgacgtga 1080
60 ccaaagccgg acacagcctg gagctgattg agcccctcat caagttccag gtgggactga 1140
61 agaagctgaa cttgcatgag gaggagcatg tcctgctcat ggccatctgc atcgtctccc 1200
62 cagatcgtcc tggggtgcag gacgccgcgc tgattgaggc catccaggac cgctgtcca 1260
63 acacactgca gacgtacatc cgctgccgcc acccgcccc gggcagccac ctgctctatg 1320
64 ccaagatgat ccagaagcta gccgacctgc gcagcctcaa tgaggagcac tccaagcagt 1380
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76 ctccctgcc tgacctgga gactttgacc ggaacgtgcc ccgatctgt ggggtgtgtg 180
77 gagaccgagc cactggcttt cacttcaatg ctatgacctg tgaaggctgc aaaggcttct 240
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80 gcatgatgaa ggagttcatt ctgacagatg aggaagtga gaggaagcgg gagatgatcc 420
81 tgaagcggaa ggaggaggag gccttgaagg acagtctgcg gcccaagctg tctgaggagc 480
82 agcagcgcac cattgccata ctgctggacg cccaccataa gacctacgac cccacctact 540
83 ccgacttctg ccagttccgg cctccagttc gtgtgaatga tgggtggagg agccatcctt 600
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90 gtggcaacca agactacaag taccgcgtca gtgacgtgac caaagccgga cacagcctgg 1020
91 agctgattga gcccctcatc aagttccagg tgggactgaa gaagctgaac ttgcatgagg 1080
92 aggagcatgt cctgctcatg gccatctgca tcgtctcccc agatcgtcct ggggtgcagg 1140
93 acgccgcgct gattgaggcc atccaggacc gcctgtccaa cacactgcag acgtacatcc 1200
94 gctgccgcca cccgcccccg ggcagccacc tgctctatgc caagatgatc cagaagctag 1260
95 ccgacctgcg cagcctcaat gaggagcact ccaagcagta ccgctgcctc tccttccagc 1320
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101 <212> TYPE: DNA

102 <213> ORGANISM: Homo sapiens

104 <400> SEQUENCE: 4

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107 ctccctgcc tgacctgga gactttgacc ggaacgtgcc ccgatctgt ggggtgtgtg 180
108 gagaccgagc cactggcttt cacttcaatg ctatgacctg tgaaggctgc aaaggcttct 240
109 tcagggtgagc cccctccca ggctctcccc agtggaagg gagggagaag aagcaagggtg 300
110 tttccatgaa gggagccctt gcatttttca catctccttc cttacaatgt ccatggaaca 360
111 tgcggcgctc acagccacag gagcaggagg gtcttggcga agcatgaagc ggaaggcact 420

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112 attcacctgc cccttcaacg gggactgccg catcaccaag gacaaccgac gccactgcca 480
113 ggcctgccgg ctcaaacgct gtgtggacat cggcatgatg aaggagttca ttctgacaga 540
114 tgaggaagtg cagaggaagc gggagatgat cctgaagcgg aaggaggagg aggccttgaa 600
115 ggacagtctg cggcccaagc tgtctgagga gcagcagcgc atcattgcca tactgctgga 660
116 cgcccaccat aagacctacg accccaccta ctccgacttc tgccagttcc ggcctccagt 720
117 tcgtgtgaat gatggtggag ggagccatcc ttccaggccc aactccagac aactcccag 780
118 cttctctggg gactcctcct cctcctgctc agatcactgt atcacctctt cagacatgat 840
119 ggactcgtcc agcttctcca atctggatct gagtgaagaa gattcagatg acccttctgt 900
120 gaccctagag ctgtcccagc tctccatgct gcccacctg gctgacctgg tcagttacag 960
121 catccaaaag gtcattggct ttgctaagat gataccagga ttcagagacc tcacctctga 1020
122 ggaccagatc gtactgctga agtcaagtgc cattgaggtc atcatgttgc gctccaatga 1080
123 gtccttcacc atggacgaca tgtcctggac ctgtggcaac caagactaca agtaccgct 1140
124 cagtgcgtg accaaagccg gacacagcct ggagctgatt gagccctca tcaagttcca 1200
125 ggtgggactg aagaagctga acttgcatga ggaggagcat gtctgtctca tggccatctg 1260
126 catcgtctcc ccagatcgtc ctgggggtgca ggacgccgcg ctgattgagg ccatccagga 1320
127 ccgctgtcc aacacactgc agacgtacat ccgctgccgc caccgcccc cgggcagcca 1380
128 cctgctctat gccaagatga tccagaagct agccgacctg cgcagcctca atgaggagca 1440
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148 <400> SEQUENCE: 6
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161 caccgcagc ccaatccatc actcagcaac tcctagacgc tggtagaaag ttcctccgag 180
162 gagcctgcc tccagtcgtg cgtgcagaag cctttgggtc tgaagtgtct gtgagacctc 240
163 acagaagagc acccctgggc tccacttacc tgccccctgc tccttcaggg atggaggcaa 300
164 tggcgggccag cacttccttg cctgacctg gagactttga ccggaacgtg ccccgatct 360
165 gtgggggtgtg tggagaccga gccactggct ttcacttcaa tgctatgacc tgtgaaggct 420
166 gcaaaggctt cttcaggcga agcatgaagc ggaaggcact attcacctgc cccttcaacg 480

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168 gtgtggacat cggcatgatg aaggagttca ttctgacaga tgaggaagtg cagaggaagc 600
169 gggagatgat cctgaagcgg aaggaggagg aggccttgaa ggacagtctg cggcccaagc 660
170 tgtctgagga gcagcagcgc atcattgccca tactgctgga cgcccacat aagacctacg 720
171 accccaccta ctccgacttc tgccagttcc ggcctccagt tcgtgtgaat gatggtggag 780
172 ggagccatcc ttccaggccc aactccagac aactcccag cttctctggg gactcctcct 840
173 cctcctgctc agatcactgt atcacctctt cagacatgat ggactcgtcc agcttctcca 900
174 atctggatct gagtgaagaa gattcagatg acccttctgt gaccctagag ctgtcccagc 960
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183 tccagaagct agccgacctg cgcagcctca atgaggagca ctccaagcag taccgctgcc 1500
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195 gg 122

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198 <211> LENGTH: 477

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205 Arg Thr Ala Gly Val Glu Glu Ala Phe Gly Ser Glu Val Ser Val Arg

206 20 25 30

207 Pro His Arg Arg Ala Pro Leu Gly Ser Thr Tyr Leu Pro Pro Ala Pro

208 35 40 45

209 Ser Gly Met Glu Ala Met Ala Ala Ser Thr Ser Leu Pro Asp Pro Gly

210 50 55 60

211 Asp Phe Asp Arg Asn Val Pro Arg Ile Cys Gly Val Cys Gly Asp Arg

212 65 70 75 80

213 Ala Thr Gly Phe His Phe Asn Ala Met Thr Cys Glu Gly Cys Lys Gly

214 85 90 95

215 Phe Phe Arg Arg Ser Met Lys Arg Lys Ala Leu Phe Thr Cys Pro Phe

216 100 105 110

217 Asn Gly Asp Cys Arg Ile Thr Lys Asp Asn Arg Arg His Cys Gln Ala

218 115 120 125

219 Cys Arg Leu Lys Arg Cys Val Asp Ile Gly Met Met Lys Glu Phe Ile

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222 145      150      155      160
223 Lys Glu Glu Glu Ala Leu Lys Asp Ser Leu Arg Pro Lys Leu Ser Glu
224      165      170      175
225 Glu Gln Gln Arg Ile Ile Ala Ile Leu Leu Asp Ala His His Lys Thr
226      180      185      190
227 Tyr Asp Pro Thr Tyr Ser Asp Phe Cys Gln Phe Arg Pro Pro Val Arg
228      195      200      205
229 Val Asn Asp Gly Gly Gly Ser His Pro Ser Arg Pro Asn Ser Arg His
230      210      215      220
231 Thr Pro Ser Phe Ser Gly Asp Ser Ser Ser Ser Cys Ser Asp His Cys
232 225      230      235      240
233 Ile Thr Ser Ser Asp Met Met Asp Ser Ser Ser Phe Ser Asn Leu Asp
234      245      250      255
235 Leu Ser Glu Glu Asp Ser Asp Asp Pro Ser Val Thr Leu Glu Leu Ser
236      260      265      270
237 Gln Leu Ser Met Leu Pro His Leu Ala Asp Leu Val Ser Tyr Ser Ile
238      275      280      285
239 Gln Lys Val Ile Gly Phe Ala Lys Met Ile Pro Gly Phe Arg Asp Leu
240      290      295      300
241 Thr Ser Glu Asp Gln Ile Val Leu Leu Lys Ser Ser Ala Ile Glu Val
242 305      310      315      320
243 Ile Met Leu Arg Ser Asn Glu Ser Phe Thr Met Asp Asp Met Ser Trp
244      325      330      335
245 Thr Cys Gly Asn Gln Asp Tyr Lys Tyr Arg Val Ser Asp Val Thr Lys
246      340      345      350
247 Ala Gly His Ser Leu Glu Leu Ile Glu Pro Leu Ile Lys Phe Gln Val
248      355      360      365
249 Gly Leu Lys Lys Leu Asn Leu His Glu Glu Glu His Val Leu Leu Met
250      370      375      380
251 Ala Ile Cys Ile Val Ser Pro Asp Arg Pro Gly Val Gln Asp Ala Ala
252 385      390      395      400
253 Leu Ile Glu Ala Ile Gln Asp Arg Leu Ser Asn Thr Leu Gln Thr Tyr
254      405      410      415
255 Ile Arg Cys Arg His Pro Pro Pro Gly Ser His Leu Leu Tyr Ala Lys
256      420      425      430
257 Met Ile Gln Lys Leu Ala Asp Leu Arg Ser Leu Asn Glu Glu His Ser
258      435      440      445
259 Lys Gln Tyr Arg Cys Leu Ser Phe Gln Pro Glu Cys Ser Met Lys Leu
260      450      455      460
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262 465      470      475
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267 <212> TYPE: PRT
268 <213> ORGANISM: Homo sapiens
270 <400> SEQUENCE: 10
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